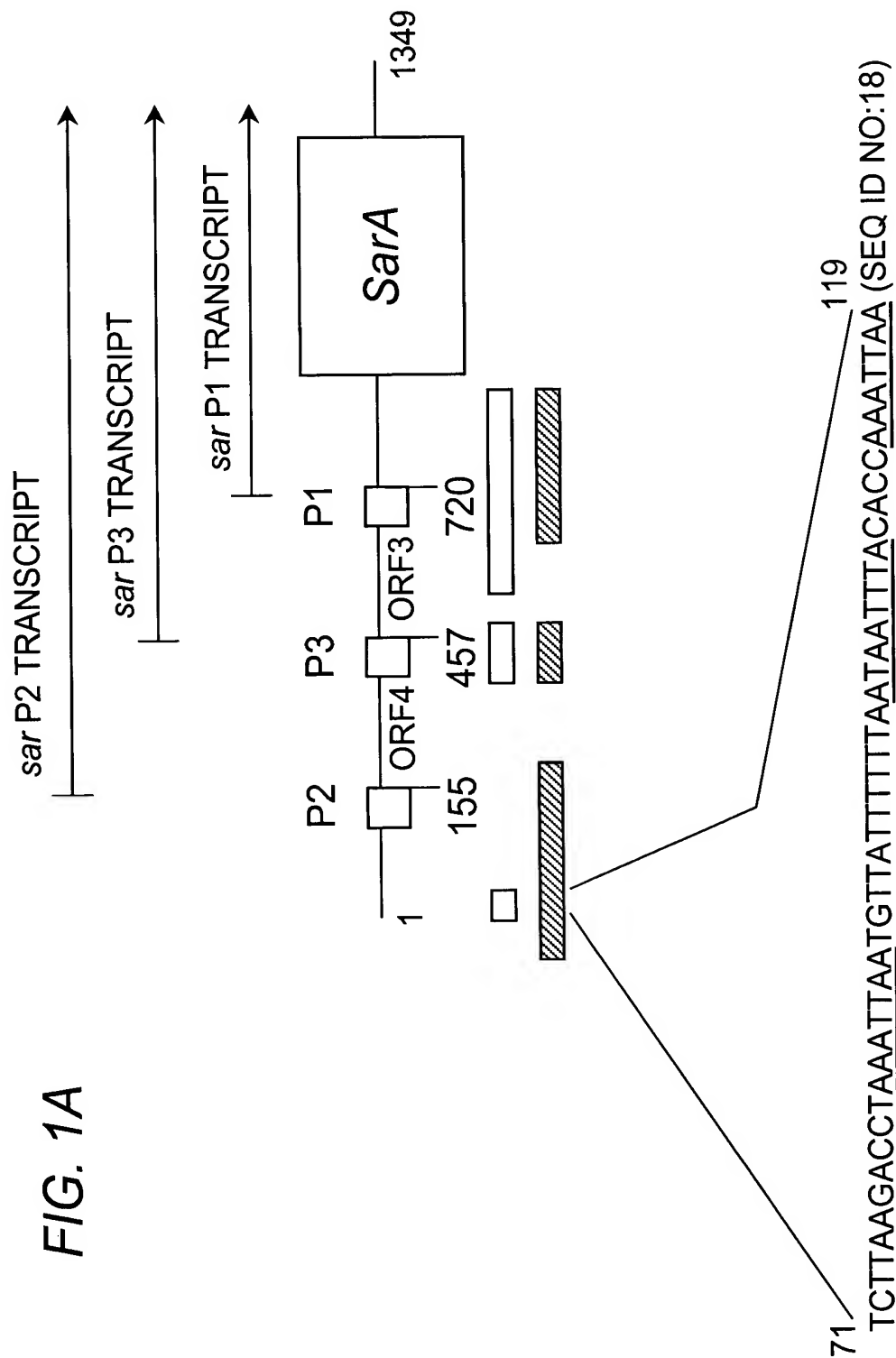
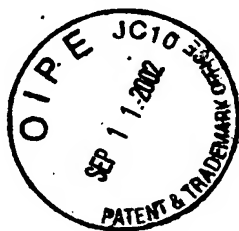


FIG. 1A





2/15

1 GTTTTCAAAA TCGGTGGAGG TGCATGAAAA AGTTATTGGG
41 CATTTTTTTGA AAATAAAAAA ATATCAATAA GTTGGAGTCA
↓START
81 TTACCGAATT TTTATACTTA TTTGTTTAGA ATGAACTTTA
-35 -10
121 TAACATAGTT GGATAGAGTT TTCGATTTAA TACATTAAAT
161 GTGAACCTTG CTACAACAAG ATGTGCATCA GAAGGAGTGG
RIBOSOME BINDING SITE
201 TTTAATAATG (SEQ ID NO:19) --sarR--TAA (SEQ ID NO:34)

FIG. 1B

	10	20	30	40
SarR	M--SKINDINDLVNATFQVKKFFRDTKKKFN	LN	YEEIYILN	
	:
SarA	MAITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLT			
	50	60	70	80
SarR	HILRSESNEISSKEIAKCSEFKPYLTKALQKLKDLKLLS			

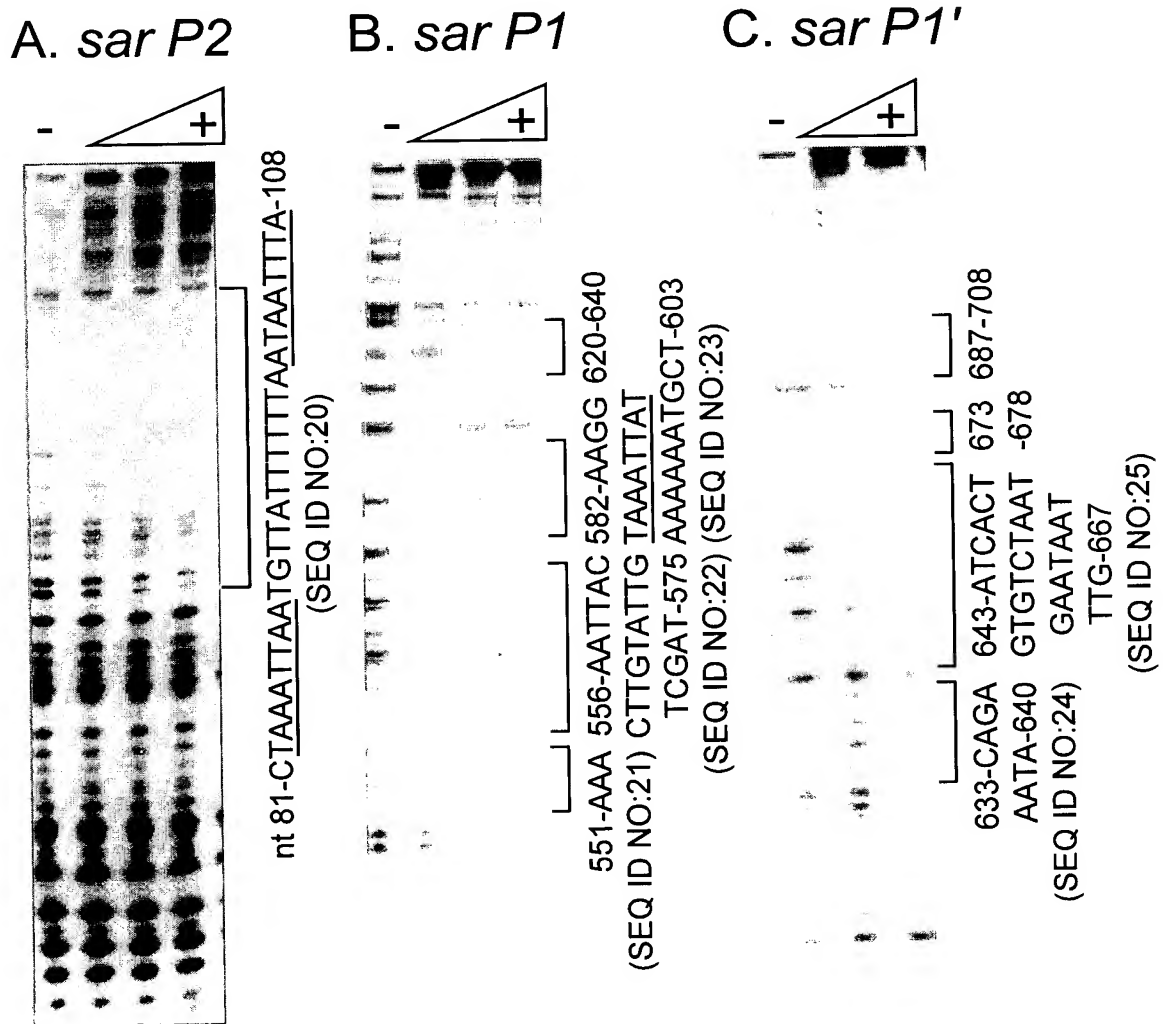
SarA	YISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFD			
	90	100	110	
SarR	QKRILQDERTVIVYVT-----DTL	KANIHKLISELEEY		

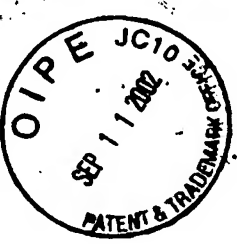
SarA	KKRNEHDERTVLILVNAQQRKKIESLLSRVNKR	ITEANNE		
SarR	IKN (SEQ ID NO:2)			
	..			
SarA	IEL (SEQ ID NO:3)			

FIG. 1C

6/15

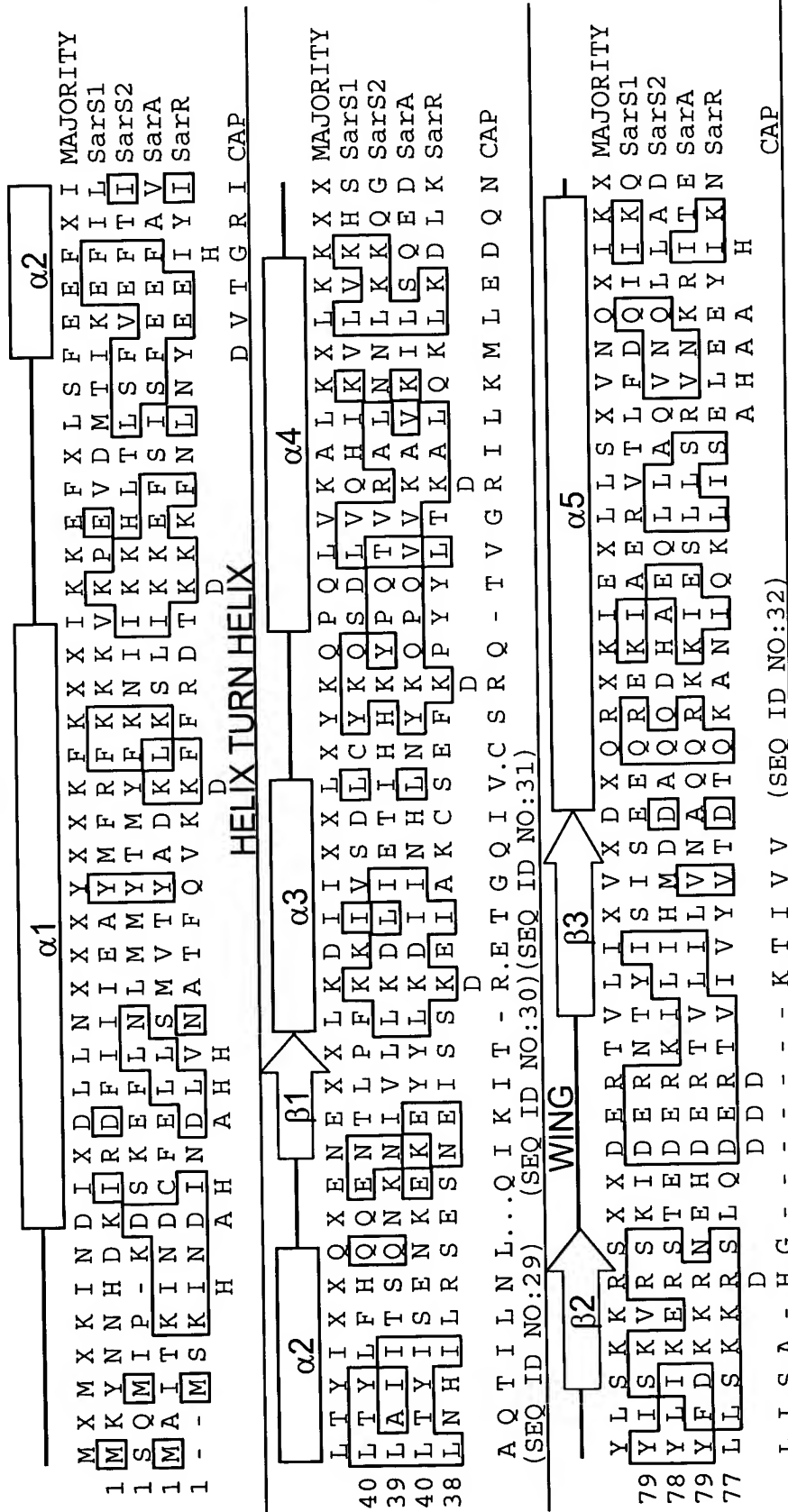
FIG. 5





13/15

FIG. 11



X N X (SEQ ID NO:26) MAJORITIVITY
119 F N - (SEQ ID NO:27) SarS1
118 - K D (SEQ ID NO:28) SarS2
119 A N (SEQ ID NO:35) SarA
117 - - - (SEQ ID NO:2) SarR